

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 10, 2006, 15:59:05 ; Search time 29.5 Seconds
 (without alignments)
 92.993 Million cell updates/sec

Title: US-10-519-890-10
 Perfect score: 32
 Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	32	100.0	6	8 ADI29056	Adi29056 Human ins
2	32	100.0	154	4 ABB64396	Abb64396 Drosophil
3	32	100.0	198	3 AAG27975	Aag27975 Arabidops
4	32	100.0	305	3 AAG30828	Aag30828 Arabidops
5	32	100.0	316	3 AAG27974	Aag27974 Arabidops
6	32	100.0	332	3 AAG30827	Aag30827 Arabidops
7	32	100.0	343	3 AAG27973	Aag27973 Arabidops
8	32	100.0	366	3 AAG30826	Aag30826 Arabidops
9	32	100.0	377	3 AAG27972	Aag27972 Arabidops
10	32	100.0	530	4 ABG29689	Abg29689 Novel hum
11	32	100.0	708	4 ABB58681	Abb58681 Drosophil
12	30	93.8	10	6 ABU52535	Abu52535 Peanut Ar

13	30	93.8	457	6	ADA33529	Ada33529	Acinetoba
14	30	93.8	1653	4	AAG98354	Aag98354	Escherich
15	30	93.8	1653	9	AED82056	Aed82056	Hyperimmu
16	30	93.8	1653	9	AED82491	Aed82491	Hyperimmu
17	29	90.6	28	8	ADF53701	Adf53701	Equine gh
18	29	90.6	28	8	ADL66842	Adl66842	Equine Gh
19	29	90.6	28	8	ADU61121	Adu61121	Equine gr
20	29	90.6	61	4	AAU44456	Aau44456	Propionib
21	29	90.6	61	6	ABM40975	Abm40975	Propionib
22	29	90.6	66	6	ABM65179	Abm65179	Propionib
23	29	90.6	79	4	ABG04784	Abg04784	Novel hum
24	29	90.6	86	6	ABM64707	Abm64707	Propionib
25	29	90.6	95	4	AAU40300	Aau40300	Propionib
26	29	90.6	95	6	ABM36819	Abm36819	Propionib
27	29	90.6	96	4	AAU64553	Aau64553	Propionib
28	29	90.6	96	6	ABM61072	Abm61072	Propionib
29	29	90.6	98	4	AAU59044	Aau59044	Propionib
30	29	90.6	98	6	ABM55563	Abm55563	Propionib
31	29	90.6	105	7	ADL06716	Adl06716	Human bra
32	29	90.6	105	7	ADL06714	Adl06714	Human bra
33	29	90.6	123	4	ABB15200	Abb15200	Human ner
34	29	90.6	127	4	ABG29587	Abg29587	Novel hum
35	29	90.6	145	7	ADE95986	Ade95986	Human uri
36	29	90.6	152	6	ABM64566	Abm64566	Propionib
37	29	90.6	156	4	AAU86633	Aau86633	Novel hum
38	29	90.6	156	7	ADB59967	Adb59967	Connectiv
39	29	90.6	158	6	ABR43445	Abr43445	Human mal
40	29	90.6	158	8	ADR46858	Adr46858	Human cys
41	29	90.6	159	6	ABU36844	Abu36844	Protein e
42	29	90.6	159	6	ABU34765	Abu34765	Protein e
43	29	90.6	165	3	AAB56382	Aab56382	Human pro
44	29	90.6	167	4	AAU31752	Aau31752	Novel hum
45	29	90.6	175	7	ABO84199	Abo84199	Pseudomon
46	29	90.6	181	2	AAW70986	Aaw70986	Amino aci
47	29	90.6	181	6	ABU33879	Abu33879	Protein e
48	29	90.6	181	8	ADS75085	Ads75085	M. avium
49	29	90.6	202	9	AEA04765	Aea04765	Indian he
50	29	90.6	211	7	ABO68295	Abo68295	Pseudomon
51	29	90.6	227	7	ABO71888	Abo71888	Pseudomon
52	29	90.6	238	9	ABM93884	Abm93884	M. xanthu
53	29	90.6	248	7	ABO80503	Abo80503	Pseudomon
54	29	90.6	258	7	ABO74247	Abo74247	Pseudomon
55	29	90.6	269	9	AEC64310	Aec64310	Poplar SG
56	29	90.6	272	8	ADT58322	Adt58322	Plant pol
57	29	90.6	301	8	ADX92889	Adx92889	Plant ful
58	29	90.6	312	7	ABO82458	Abo82458	Pseudomon
59	29	90.6	316	8	ADN26248	Adn26248	Bacterial
60	29	90.6	326	7	ABO76724	Abo76724	Pseudomon
61	29	90.6	326	8	ABO58549	Abo58549	Human gen
62	29	90.6	335	8	ADY11082	Ady11082	Plant ful
63	29	90.6	349	4	ABB62556	Abb62556	Drosophil
64	29	90.6	350	7	ABO77322	Abo77322	Pseudomon
65	29	90.6	365	8	ADY09180	Ady09180	Plant ful
66	29	90.6	367	8	ADO51711	Ado51711	Streptomy
67	29	90.6	386	7	ABO70481	Abo70481	Pseudomon
68	29	90.6	388	6	AAE32782	Aae32782	Mycobacte
69	29	90.6	392	4	ABG25625	Abg25625	Novel hum
70	29	90.6	392	4	ABG25990	Abg25990	Novel hum
71	29	90.6	392	4	ABG25082	Abg25082	Novel hum
72	29	90.6	398	8	ADX79724	Adx79724	Plant ful
73	29	90.6	411	2	AAW94474	Aaw94474	Human Ihh

74	29	90.6	411	2	AAy05860	Aay05860	Human	Ind
75	29	90.6	411	2	AAW97763	Aaw97763	Human	Ind
76	29	90.6	411	2	AAy05516	Aay05516	Human	Ind
77	29	90.6	411	3	AAy96249	Aay96249	Human	Ihh
78	29	90.6	411	3	AAy70682	Aay70682	Human	Ind
79	29	90.6	411	3	AAy95287	Aay95287	Human	Ind
80	29	90.6	411	3	AAy95978	Aay95978	Human	Ind
81	29	90.6	411	4	AAB84675	Aab84675	Amino	aci
82	29	90.6	411	4	AAB60266	Aab60266	Human	Ind
83	29	90.6	411	4	AAE04688	Aae04688	Human	ind
84	29	90.6	411	4	AAB85091	Aab85091	Human	ind
85	29	90.6	411	4	AAG65749	Aag65749	Human	ind
86	29	90.6	411	5	AAE14298	Aae14298	Human	Ind
87	29	90.6	411	5	AAO20924	Aao20924	Human	Ihh
88	29	90.6	411	5	AAU99484	Aau99484	Human	Ind
89	29	90.6	411	7	ADK66382	Adk66382	Human	ind
90	29	90.6	411	7	ADL06710	Adl06710	Human	bra
91	29	90.6	411	7	ADL06712	Adl06712	Human	bra
92	29	90.6	411	8	ADH56644	Adh56644	Human	Ind
93	29	90.6	411	8	ADK82143	Adk82143	Human	Ind
94	29	90.6	411	8	ADR03323	Adr03323	Human	Ind
95	29	90.6	411	9	ADU81698	Adu81698	Human	Ind
96	29	90.6	411	9	ADZ72181	Adz72181	Human	ind
97	29	90.6	411	9	ADZ76232	Adz76232	Human	Ind
98	29	90.6	411	9	AEB22478	Aeb22478	Human	Ind
99	29	90.6	411	9	AED67915	Aed67915	Human	ind
100	29	90.6	411	10	AEE84665	Aee84665	Indian	he
101	29	90.6	413	5	ABG91520	Abg91520	Purine/py	
102	29	90.6	413	8	ADS43190	Ads43190	Bacterial	
103	29	90.6	416	4	AAB96271	Aab96271	Putative	
104	29	90.6	426	4	AAU42357	Aau42357	Propionib	
105	29	90.6	426	6	ABM38876	Abm38876	Propionib	
106	29	90.6	430	3	AAG49406	Aag49406	Arabidops	
107	29	90.6	436	7	ABO72128	Abo72128	Pseudomon	
108	29	90.6	437	8	ADN73531	Adn73531	Thale cre	
109	29	90.6	438	8	ADY07348	Ady07348	Plant ful	
110	29	90.6	446	3	AAG49405	Aag49405	Arabidops	
111	29	90.6	452	3	AAG49404	Aag49404	Arabidops	
112	29	90.6	456	7	ABO81779	Abo81779	Pseudomon	
113	29	90.6	473	7	ABO76296	Abo76296	Pseudomon	
114	29	90.6	498	8	ADX93481	Adx93481	Plant ful	
115	29	90.6	553	7	ABO83875	Abo83875	Pseudomon	
116	29	90.6	568	7	ABO74518	Abo74518	Pseudomon	
117	29	90.6	568	7	ABO78805	Abo78805	Pseudomon	
118	29	90.6	574	7	ABO70709	Abo70709	Pseudomon	
119	29	90.6	589	6	ABU35784	Abu35784	Protein e	
120	29	90.6	605	7	ABO70716	Abo70716	Pseudomon	
121	29	90.6	608	4	AAG91551	Aag91551	C glutami	
122	29	90.6	626	4	ABB64471	Abb64471	Drosophil	
123	29	90.6	647	8	ADU01120	Adu01120	Human pro	
124	29	90.6	647	8	ADU15502	Adu15502	Novel hum	
125	29	90.6	672	7	ABO68195	Abo68195	Pseudomon	
126	29	90.6	682	7	ABO74251	Abo74251	Pseudomon	
127	29	90.6	705	7	ABO79607	Abo79607	Pseudomon	
128	29	90.6	726	4	ABB64481	Abb64481	Drosophil	
129	29	90.6	827	7	ADF55472	Adf55472	Human nov	
130	29	90.6	846	4	ABG11594	Abg11594	Novel hum	
131	29	90.6	852	6	AAO30995	Aao30995	Human tra	
132	29	90.6	871	7	AEB86062	Aeb86062	Protein d	
133	29	90.6	1008	7	ABO80673	Abo80673	Pseudomon	
134	29	90.6	1020	7	ABO80124	Abo80124	Pseudomon	

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:02:44 ; Search time 6.25 Seconds
 (without alignments)
 92.368 Million cell updates/sec

Title: US-10-519-890-10

Perfect score: 32

Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	32	100.0	259	2	G82601	conserved hypothet
2	32	100.0	366	2	D96649	hypothetical prote
3	30	93.8	445	2	D84385	oligopeptide ABC t
4	30	93.8	493	2	T07911	catalase (EC 1.11.
5	30	93.8	1644	2	AC0823	probable lipoprote
6	30	93.8	1653	2	B91052	hypothetical prote
7	30	93.8	1653	2	F85896	hypothetical prote
8	30	93.8	1653	2	G65028	hypothetical prote
9	29	90.6	118	2	D72609	hypothetical prote
10	29	90.6	159	2	B70881	probable dfrA prot
11	29	90.6	225	2	A75425	hypothetical prote
12	29	90.6	388	2	G70729	hypothetical prote
13	29	90.6	413	2	H75070	sugar-phosphate nu
14	29	90.6	423	2	T05396	hypothetical prote
15	29	90.6	423	2	T05343	hypothetical prote
16	29	90.6	431	2	T33287	hypothetical prote
17	29	90.6	475	2	T36921	hypothetical prote
18	29	90.6	482	2	G70063	cardiolipin syntha

19	29	90.6	589	1	S42047	aspartate-tRNA lig
20	29	90.6	901	2	T20122	hypothetical prote
21	29	90.6	928	2	T24868	hypothetical prote
22	29	90.6	1207	2	T00378	KIAA0641 protein -
23	29	90.6	2109	2	I38414	transcription fact
24	29	90.6	2670	2	T37919	GCN1 homolog - fis
25	28	87.5	117	1	A59316	ghrelin precursor
26	28	87.5	117	1	B59316	ghrelin precursor
27	28	87.5	143	2	S63735	HIV-1 retropepsin
28	28	87.5	424	1	B40905	inhibin beta-A cha
29	28	87.5	424	1	S31440	inhibin beta-A cha
30	28	87.5	424	1	WFPGBA	inhibin beta-A cha
31	28	87.5	425	1	S50898	inhibin beta-A cha
32	28	87.5	425	2	I47072	inhibin beta-A cha
33	28	87.5	426	1	B24248	inhibin beta-A cha
34	28	87.5	452	2	JC4100	hydroxyindole O-me
35	28	87.5	540	2	A75250	carboxylesterase,
36	28	87.5	547	2	E70720	probable ilvG prot
37	28	87.5	565	2	T08794	hypothetical prote
38	28	87.5	600	2	D83430	type III secretion
39	28	87.5	755	2	B75346	probable competenc
40	28	87.5	772	2	H86492	Pmp_3 [imported] -
41	28	87.5	855	2	C82983	hypothetical prote
42	28	87.5	1039	2	T35878	hypothetical prote
43	28	87.5	1123	2	T47687	adaptor protein/ a
44	28	87.5	1260	2	A86323	protein F14D16.3 [
45	28	87.5	1426	2	A99580	hypothetical prote
46	28	87.5	1846	2	T33079	hypothetical prote
47	28	87.5	2247	2	T16637	hypothetical prote
48	27	84.4	50	4	IMBP13	hypothetical immun
49	27	84.4	107	1	WMLJSP	S1 protein - human
50	27	84.4	121	2	T08717	hypothetical prote
51	27	84.4	127	2	I57612	hypothetical prote
52	27	84.4	127	2	T14797	hypothetical prote
53	27	84.4	142	2	G86398	protein F17L21.8 [
54	27	84.4	154	2	E64504	hypothetical prote
55	27	84.4	193	2	A33562	pol polyprotein -
56	27	84.4	210	2	T41082	probable mitochond
57	27	84.4	231	2	D75412	hypothetical prote
58	27	84.4	270	2	JC7631	K+ channel-interac
59	27	84.4	304	2	A33274	insulin-like growt
60	27	84.4	305	2	JN0508	insulin-like growt
61	27	84.4	305	2	I48601	insulin-like growt
62	27	84.4	310	2	A60967	insulin-like growt
63	27	84.4	317	2	I46916	insulin-like growt
64	27	84.4	328	1	A41927	insulin-like growt
65	27	84.4	334	1	T51050	probable phosphopr
66	27	84.4	353	2	H87545	vanillate O-demeth
67	27	84.4	353	2	A83609	probable periplasm
68	27	84.4	366	1	DEBSIC	3-isopropylmalate
69	27	84.4	391	2	T36739	hypothetical prote
70	27	84.4	402	2	T52522	hypothetical prote
71	27	84.4	404	2	F71324	probable gcpE prot
72	27	84.4	414	2	B98354	hypothetical prote
73	27	84.4	446	2	F69053	conserved hypothet
74	27	84.4	463	2	S28469	phosphomannomutase
75	27	84.4	467	2	T01462	hypothetical prote
76	27	84.4	492	2	AC0768	probable transmemb
77	27	84.4	502	2	T27908	hypothetical prote
78	27	84.4	520	2	H64510	hypothetical prote
79	27	84.4	537	2	C71008	probable proline p

80	27	84.4	595	2	T04438	hypothetical prote
81	27	84.4	609	2	F70512	probable ATPase -
82	27	84.4	609	2	S72845	H+-transporting tw
83	27	84.4	665	2	JC7191	85K c-Cbl-interact
84	27	84.4	700	2	A61527	stonustoxin beta c
85	27	84.4	705	2	T35165	probable integral
86	27	84.4	738	2	AB2899	primosomal protein
87	27	84.4	763	2	C97674	primosomal protein
88	27	84.4	779	2	G87573	xanthine dehydroge
89	27	84.4	789	1	B4AGA6	virB4 protein prec
90	27	84.4	793	2	S67070	GAC1 protein - yea
91	27	84.4	825	2	AC0039	glycerol-3-phospha
92	27	84.4	844	2	F86231	hypothetical prote
93	27	84.4	970	2	E70533	probable sulfatase
94	27	84.4	1056	2	G84865	hypothetical prote
95	27	84.4	1083	1	S53048	alpha-mannosidase
96	27	84.4	1157	1	GNLJLK	pol polyprotein -
97	27	84.4	1161	2	S18738	pol protein - simi
98	27	84.4	1293	2	S42402	xeroderma pigmento
99	27	84.4	1303	2	B96805	hypothetical prote
100	27	84.4	1336	2	T17479	hypothetical prote
101	27	84.4	1830	1	S19188	myosin-V - chicken
102	27	84.4	2314	2	T28698	hypothetical prote
103	27	84.4	2342	2	T13412	hypothetical prote
104	27	84.4	2531	2	T16743	hypothetical prote
105	27	84.4	3161	2	T30342	protein HMWP1 - Ye
106	27	84.4	5126	2	S40450	ryanodine receptor
107	26	81.2	82	2	T10149	probable hexose tr
108	26	81.2	112	2	D72654	hypothetical prote
109	26	81.2	114	2	E70757	hypothetical prote
110	26	81.2	116	2	D97573	hypothetical prote
111	26	81.2	124	2	B45945	histone H2B - rat
112	26	81.2	125	2	S26185	histone H2B - rat
113	26	81.2	131	2	S42592	urease (EC 3.5.1.5
114	26	81.2	134	2	T12584	asparagine synthas
115	26	81.2	150	2	T35638	hypothetical prote
116	26	81.2	161	2	S39483	ubiquitin-conjugat
117	26	81.2	183	2	C55663	oligodendrocyte-sp
118	26	81.2	214	2	D64442	conserved hypothet
119	26	81.2	232	2	B96803	hypothetical prote
120	26	81.2	235	2	G81138	probable succinate
121	26	81.2	237	2	AF0645	probable regulator
122	26	81.2	239	2	T36995	hypothetical prote
123	26	81.2	240	2	T35972	hypothetical prote
124	26	81.2	252	2	JC2399	PMS4 homolog misma
125	26	81.2	259	2	E82191	probable nicotinat
126	26	81.2	266	2	A86288	protein F9L1.30 [i
127	26	81.2	267	2	H84396	hypothetical prote
128	26	81.2	271	2	T36040	hypothetical prote
129	26	81.2	273	2	B99816	hypothetical prote
130	26	81.2	273	2	F85675	hypothetical prote
131	26	81.2	279	2	E64856	hypothetical prote
132	26	81.2	304	1	SYSMPG	dTDP-dihydrostrept
133	26	81.2	306	2	B97315	aldo/keto reductas
134	26	81.2	322	2	A70607	hypothetical prote
135	26	81.2	328	2	E81089	glucokinase (EC 2.
136	26	81.2	330	2	T22411	hypothetical prote
137	26	81.2	349	2	AB1715	oxidoreductase hom
138	26	81.2	349	2	AG1344	oxidoreductase hom
139	26	81.2	363	2	C44971	histidine-rich kno
140	26	81.2	364	2	A70474	conserved hypothet

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:03:03 ; Search time 11.5 Seconds
 (without alignments)
 45.668 Million cell updates/sec

Title: US-10-519-890-10
 Perfect score: 32
 Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	56	2	US-09-270-767-34420	Sequence 34420, A
2	32	100.0	56	2	US-09-270-767-49637	Sequence 49637, A
3	32	100.0	182	2	US-09-270-767-43696	Sequence 43696, A
4	30	93.8	457	2	US-09-328-352-4816	Sequence 4816, Ap
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130	28	87.5	28	4	US-10-276-392-13	Sequence 13, Appl
131	28	87.5	28	4	US-10-276-392-14	Sequence 14, Appl
132	28	87.5	28	4	US-10-276-392-15	Sequence 15, Appl
133	28	87.5	28	4	US-10-276-392-16	Sequence 16, Appl
134	28	87.5	28	4	US-10-276-392-17	Sequence 17, Appl
135	28	87.5	28	4	US-10-276-392-18	Sequence 18, Appl
136	28	87.5	28	4	US-10-276-392-19	Sequence 19, Appl
137	28	87.5	28	4	US-10-276-392-20	Sequence 20, Appl
138	28	87.5	28	4	US-10-276-392-21	Sequence 21, Appl

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:04:43 ; Search time 3.5 Seconds
 (without alignments)
 45.998 Million cell updates/sec

Title: US-10-519-890-10
 Perfect score: 32
 Sequence: 1 PAKLRP 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters: 112942

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	90.6	86	6	US-10-953-349-40084	Sequence 40084, A
2	29	90.6	131	6	US-10-449-902-47275	Sequence 47275, A
3	29	90.6	153	6	US-10-953-349-25819	Sequence 25819, A
4	29	90.6	175	6	US-10-953-349-25818	Sequence 25818, A
5	29	90.6	318	6	US-10-953-349-26735	Sequence 26735, A
6	29	90.6	344	6	US-10-449-902-50913	Sequence 50913, A
7	29	90.6	686	6	US-10-449-902-45827	Sequence 45827, A
8	28	87.5	28	7	US-11-257-498-33	Sequence 33, Appl
9	28	87.5	28	7	US-11-257-498-34	Sequence 34, Appl
10	28	87.5	28	7	US-11-257-498-35	Sequence 35, Appl
11	28	87.5	28	7	US-11-257-498-40	Sequence 40, Appl
12	28	87.5	117	7	US-11-255-699-6	Sequence 6, Appli
13	28	87.5	121	7	US-11-356-823-21	Sequence 21, Appl
14	28	87.5	341	6	US-10-953-349-31800	Sequence 31800, A

15	28	87.5	377	6	US-10-953-349-31798	Sequence 31798, A
16	28	87.5	388	6	US-10-953-349-32611	Sequence 32611, A
17	28	87.5	555	7	US-11-293-697-4766	Sequence 4766, Ap
18	28	87.5	755	6	US-10-449-902-47527	Sequence 47527, A
19	27	84.4	38	6	US-10-449-902-29624	Sequence 29624, A
20	27	84.4	38	6	US-10-449-902-34229	Sequence 34229, A
21	27	84.4	75	6	US-10-953-349-10327	Sequence 10327, A
22	27	84.4	160	6	US-10-449-902-45257	Sequence 45257, A
23	27	84.4	209	6	US-10-449-902-37987	Sequence 37987, A
24	27	84.4	291	6	US-10-449-902-52072	Sequence 52072, A
25	27	84.4	311	6	US-10-449-902-36921	Sequence 36921, A
26	27	84.4	311	6	US-10-449-902-47134	Sequence 47134, A
27	27	84.4	328	6	US-10-505-928-191	Sequence 191, App
28	27	84.4	338	7	US-11-174-307B-3180	Sequence 3180, Ap
29	27	84.4	352	7	US-11-174-307B-3460	Sequence 3460, Ap
30	27	84.4	599	7	US-11-293-697-3692	Sequence 3692, Ap
31	27	84.4	622	6	US-10-449-902-54041	Sequence 54041, A
32	27	84.4	710	6	US-10-449-902-55139	Sequence 55139, A
33	27	84.4	751	6	US-10-449-902-55410	Sequence 55410, A
34	27	84.4	1164	7	US-11-294-155-8	Sequence 8, Appli
35	27	84.4	1202	7	US-11-294-155-22	Sequence 22, Appl
36	26	81.2	47	7	US-11-116-142B-12	Sequence 12, Appl
37	26	81.2	112	6	US-10-953-349-16419	Sequence 16419, A
38	26	81.2	161	6	US-10-953-349-27684	Sequence 27684, A
39	26	81.2	161	6	US-10-449-902-56689	Sequence 56689, A
40	26	81.2	180	6	US-10-953-349-27683	Sequence 27683, A
41	26	81.2	185	6	US-10-953-349-39035	Sequence 39035, A
42	26	81.2	192	6	US-10-953-349-39034	Sequence 39034, A
43	26	81.2	198	6	US-10-449-902-34937	Sequence 34937, A
44	26	81.2	204	7	US-11-293-697-4233	Sequence 4233, Ap
45	26	81.2	216	6	US-10-953-349-33317	Sequence 33317, A
46	26	81.2	246	6	US-10-449-902-51236	Sequence 51236, A
47	26	81.2	250	7	US-11-293-697-4069	Sequence 4069, Ap
48	26	81.2	259	6	US-10-953-349-33316	Sequence 33316, A
49	26	81.2	261	6	US-10-449-902-31054	Sequence 31054, A
50	26	81.2	261	6	US-10-449-902-52282	Sequence 52282, A
51	26	81.2	293	6	US-10-449-902-30804	Sequence 30804, A
52	26	81.2	308	6	US-10-953-349-26114	Sequence 26114, A
53	26	81.2	310	6	US-10-449-902-31942	Sequence 31942, A
54	26	81.2	310	6	US-10-449-902-45792	Sequence 45792, A
55	26	81.2	337	6	US-10-953-349-39284	Sequence 39284, A
56	26	81.2	339	6	US-10-953-349-34788	Sequence 34788, A
57	26	81.2	357	6	US-10-449-902-49470	Sequence 49470, A
58	26	81.2	362	6	US-10-953-349-33315	Sequence 33315, A
59	26	81.2	363	6	US-10-449-902-43360	Sequence 43360, A
60	26	81.2	364	6	US-10-953-349-26113	Sequence 26113, A
61	26	81.2	369	6	US-10-953-349-28327	Sequence 28327, A
62	26	81.2	379	6	US-10-449-902-48349	Sequence 48349, A
63	26	81.2	384	7	US-11-293-697-2595	Sequence 2595, Ap
64	26	81.2	395	6	US-10-953-349-26112	Sequence 26112, A
65	26	81.2	400	6	US-10-953-349-28326	Sequence 28326, A
66	26	81.2	401	6	US-10-953-349-35747	Sequence 35747, A
67	26	81.2	403	6	US-10-449-902-48024	Sequence 48024, A
68	26	81.2	431	6	US-10-953-349-35746	Sequence 35746, A
69	26	81.2	435	7	US-11-174-307B-3160	Sequence 3160, Ap
70	26	81.2	445	6	US-10-449-902-45173	Sequence 45173, A
71	26	81.2	462	6	US-10-953-349-35745	Sequence 35745, A
72	26	81.2	464	6	US-10-449-902-48010	Sequence 48010, A
73	26	81.2	499	6	US-10-449-902-44934	Sequence 44934, A
74	26	81.2	501	6	US-10-449-902-37975	Sequence 37975, A
75	26	81.2	572	6	US-10-449-902-37842	Sequence 37842, A

76	26	81.2	661	6	US-10-449-902-42670	Sequence 42670, A
77	26	81.2	681	7	US-11-258-767-13	Sequence 13, Appl
78	26	81.2	695	7	US-11-258-767-26	Sequence 26, Appl
79	26	81.2	707	7	US-11-258-767-14	Sequence 14, Appl
80	26	81.2	707	7	US-11-258-767-20	Sequence 20, Appl
81	26	81.2	708	7	US-11-258-767-16	Sequence 16, Appl
82	26	81.2	708	7	US-11-258-767-19	Sequence 19, Appl
83	26	81.2	708	7	US-11-258-767-22	Sequence 22, Appl
84	26	81.2	708	7	US-11-258-767-23	Sequence 23, Appl
85	26	81.2	708	7	US-11-258-767-24	Sequence 24, Appl
86	26	81.2	708	7	US-11-258-767-28	Sequence 28, Appl
87	26	81.2	708	7	US-11-258-767-29	Sequence 29, Appl
88	26	81.2	708	7	US-11-258-767-32	Sequence 32, Appl
89	26	81.2	708	7	US-11-258-767-35	Sequence 35, Appl
90	26	81.2	708	7	US-11-258-767-38	Sequence 38, Appl
91	26	81.2	708	7	US-11-258-767-39	Sequence 39, Appl
92	26	81.2	709	7	US-11-258-767-31	Sequence 31, Appl
93	26	81.2	710	7	US-11-258-767-33	Sequence 33, Appl
94	26	81.2	711	7	US-11-258-767-12	Sequence 12, Appl
95	26	81.2	711	7	US-11-258-767-15	Sequence 15, Appl
96	26	81.2	711	7	US-11-258-767-17	Sequence 17, Appl
97	26	81.2	711	7	US-11-258-767-18	Sequence 18, Appl
98	26	81.2	711	7	US-11-258-767-21	Sequence 21, Appl
99	26	81.2	711	7	US-11-258-767-27	Sequence 27, Appl
100	26	81.2	711	7	US-11-258-767-30	Sequence 30, Appl
101	26	81.2	711	7	US-11-258-767-34	Sequence 34, Appl
102	26	81.2	720	6	US-10-505-928-383	Sequence 383, App
103	26	81.2	761	6	US-10-449-902-55285	Sequence 55285, A
104	26	81.2	777	6	US-10-449-902-54016	Sequence 54016, A
105	26	81.2	883	7	US-11-297-383-11	Sequence 11, Appl
106	26	81.2	1226	7	US-11-221-332-88	Sequence 88, Appl
107	26	81.2	1674	6	US-10-511-937-2587	Sequence 2587, Ap
108	25	78.1	21	6	US-10-781-841-52	Sequence 52, Appl
109	25	78.1	66	6	US-10-449-902-52748	Sequence 52748, A
110	25	78.1	74	6	US-10-953-349-28164	Sequence 28164, A
111	25	78.1	100	7	US-11-197-712-472	Sequence 472, App
112	25	78.1	105	6	US-10-449-902-53581	Sequence 53581, A
113	25	78.1	108	6	US-10-449-902-42732	Sequence 42732, A
114	25	78.1	109	7	US-11-197-712-471	Sequence 471, App
115	25	78.1	132	6	US-10-449-902-29137	Sequence 29137, A
116	25	78.1	132	6	US-10-449-902-48826	Sequence 48826, A
117	25	78.1	145	6	US-10-449-902-47086	Sequence 47086, A
118	25	78.1	163	6	US-10-953-349-15516	Sequence 15516, A
119	25	78.1	169	6	US-10-953-349-38494	Sequence 38494, A
120	25	78.1	195	6	US-10-449-902-29284	Sequence 29284, A
121	25	78.1	198	6	US-10-449-902-29924	Sequence 29924, A
122	25	78.1	198	6	US-10-449-902-48938	Sequence 48938, A
123	25	78.1	201	6	US-10-449-902-29726	Sequence 29726, A
124	25	78.1	206	6	US-10-953-349-35948	Sequence 35948, A
125	25	78.1	207	6	US-10-953-349-15515	Sequence 15515, A
126	25	78.1	219	6	US-10-370-959-43	Sequence 43, Appl
127	25	78.1	222	6	US-10-449-902-39894	Sequence 39894, A
128	25	78.1	233	6	US-10-953-349-35947	Sequence 35947, A
129	25	78.1	239	7	US-11-006-802-1	Sequence 1, Appli
130	25	78.1	239	7	US-11-006-802-5	Sequence 5, Appli
131	25	78.1	247	6	US-10-449-902-37903	Sequence 37903, A
132	25	78.1	249	6	US-10-449-902-47790	Sequence 47790, A
133	25	78.1	251	6	US-10-471-571A-1320	Sequence 1320, Ap
134	25	78.1	258	6	US-10-449-902-54726	Sequence 54726, A
135	25	78.1	266	7	US-11-174-307B-4916	Sequence 4916, Ap
136	25	78.1	268	6	US-10-953-349-16740	Sequence 16740, A

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:02:15 ; Search time 123.75 Seconds
 (without alignments)
 134.548 Million cell updates/sec

Title: US-10-519-890-16
 Perfect score: 98
 Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	93	94.9	141	2	Q5IF07_HORSE	Q5if07 equus cabal
2	93	94.9	175	2	Q6LDF9_RAT	Q6ldf9 rattus norv
3	93	94.9	304	1	IBP2_RAT	P12843 rattus norv
4	93	94.9	304	2	Q569C7_RAT	Q569c7 rattus norv
5	93	94.9	316	1	IBP2_PIG	P24853 sus scrofa
6	93	94.9	317	1	IBP2_BOVIN	P13384 bos taurus
7	93	94.9	317	1	IBP2_SHEEP	Q29400 ovis aries
8	93	94.9	328	1	IBP2_HUMAN	P18065 homo sapien
9	90	91.8	75	2	Q7T186_CHICK	Q7t186 gallus gall
10	90	91.8	209	2	Q802T1_CHICK	Q802t1 gallus gall
11	90	91.8	311	1	IBP2_CHICK	P49705 gallus gall
12	87	88.8	304	2	Q9D057_MOUSE	Q9d057 mus musculu
13	87	88.8	305	1	IBP2_MOUSE	P47877 mus musculu
14	87	88.8	305	2	Q91VK7_MOUSE	Q91vk7 mus musculu
15	75	76.5	281	2	Q5XHC5_XENLA	Q5xhc5 xenopus lae
16	74	75.5	87	2	Q90ZR1_ORYLA	Q90zr1 oryzias lat
17	74	75.5	271	2	Q4SM92_TETNG	Q4sm92 tetraodon n
18	70	71.4	262	2	Q8JHX6_BRARE	Q8jhx6 brachydanio
19	70	71.4	262	2	Q90YJ7_BRARE	Q90yj7 brachydanio
20	70	71.4	276	1	IBP2_BRARE	Q9pth3 brachydanio

21	69	70.4	283	2	Q3I344_ONCMY	Q3i344 oncorhynchu
22	67	68.4	286	2	Q8UVU5_SPAAU	Q8uvu5 sparus aura
23	61	62.2	145	2	Q9DFM6_GILMI	Q9dfm6 gillichthys
24	60	61.2	236	2	Q4SK70_TETNG	Q4sk70 tetraodon n
25	60	61.2	283	2	Q3I346_ONCMY	Q3i346 oncorhynchu
26	52	53.1	269	2	Q6PAX6_XENLA	Q6pax6 xenopus lae
27	52	53.1	390	2	Q3XR38_9PROT	Q3xr38 magnetococc
28	50	51.0	267	2	Q499C6_XENTR	Q499c6 xenopus tro
29	49	50.0	244	2	Q3HWG3_ONCMY	Q3hwg3 oncorhynchu
30	49	50.0	244	2	Q5GBG2_ONCTS	Q5gbg2 oncorhynchu
31	48	49.0	95	2	Q9GK34_SHEEP	Q9gk34 ovis aries
32	48	49.0	170	2	Q9ZHQ8_HELPY	Q9zhq8 helicobacte
33	48	49.0	199	2	Q9S609_HELPY	Q9s609 helicobacte
34	48	49.0	201	2	Q9ZIR8_HELPY	Q9zir8 helicobacte
35	48	49.0	205	2	Q9S608_HELPY	Q9s608 helicobacte
36	48	49.0	223	2	Q9ZHQ9_HELPY	Q9zhq9 helicobacte
37	48	49.0	234	2	Q9F7U4_HELPY	Q9f7u4 helicobacte
38	48	49.0	235	2	Q306Y7_HELPY	Q306y7 helicobacte
39	48	49.0	235	2	Q6PRE9_HELPY	Q6pre9 helicobacte
40	48	49.0	235	2	Q8KKD6_HELPY	Q8kkd6 helicobacte
41	48	49.0	236	2	Q48249_HELPY	Q48249 helicobacte
42	48	49.0	239	2	Q83Z34_HELPY	Q83z34 helicobacte
43	48	49.0	240	2	Q3LR56_HELPY	Q3lr56 helicobacte
44	48	49.0	252	2	O68899_HELPY	O68899 helicobacte
45	48	49.0	272	1	IBP1_RAT	P21743 rattus norv
46	48	49.0	272	2	Q5SVY8_MOUSE	Q5svy8 mus musculu
47	48	49.0	272	2	Q6Q484_SPETR	Q6q484 spermophilu
48	48	49.0	272	2	Q91WV8_MOUSE	Q91wv8 mus musculu
49	47	48.0	132	2	Q53VM7_PIG	Q53vm7 sus scrofa
50	47	48.0	262	1	IBP1_PIG	Q75zp3 sus scrofa
51	47	48.0	263	1	IBP1_BOVIN	P24591 bos taurus
52	47	48.0	263	2	Q2T9Z3_BOVIN	Q2t9z3 bos taurus
53	46	46.9	115	2	Q5IF08_HORSE	Q5if08 equus cabal
54	46	46.9	259	1	IBP1_HUMAN	P08833 homo sapien
55	46	46.9	259	2	Q6PEY6_HUMAN	Q6pey6 homo sapien
56	46	46.9	269	2	Q6PN72_CHICK	Q6pn72 gallus gall
57	46	46.9	291	2	Q4RMT3_TETNG	Q4rmt3 tetraodon n
58	46	46.9	358	2	Q3Q7C2_9GAMM	Q3q7c2 shewanella
59	45	45.9	272	1	IBP1_MOUSE	P47876 mus musculu
60	45	45.9	5317	2	Q8TA74_HEMPU	Q8ta74 hemicentrot
61	44	44.9	126	2	Q5Z3W4_NOCFA	Q5z3w4 nocardia fa
62	44	44.9	272	1	TRPA_LEGPA	Q5x5q1 legionella
63	44	44.9	272	1	TRPA_LEGPH	Q5zvy3 legionella
64	44	44.9	272	1	TRPA_LEGPL	Q5wx31 legionella
65	44	44.9	330	2	Q53LV6_ORYSA	Q53lv6 oryza sativ
66	44	44.9	358	2	Q33QD9_9GAMM	Q33qd9 shewanella
67	44	44.9	392	2	Q3QQL6_9RHOB	Q3qq16 silicibacte
68	44	44.9	393	2	Q5LMZ5_SILPO	Q5lmz5 silicibacte
69	44	44.9	596	2	Q8DIY3_SYNEL	Q8diy3 synechococc
70	44	44.9	1323	2	Q6BZ91_DEBHA	Q6bz91 debaryomyce
71	43	43.9	246	2	Q5LIJ9_BACFN	Q5lij9 bacteroides
72	43	43.9	246	2	Q64ZM3_BACFR	Q64zm3 bacteroides
73	43	43.9	352	2	Q8GSM4_LYCES	Q8gsm4 lycopersico
74	43	43.9	358	2	Q2WW93_9GAMM	Q2ww93 shewanella
75	43	43.9	358	2	Q2ZLP2_SHEPU	Q2zlp2 shewanella
76	43	43.9	364	2	Q613A9_CAEBR	Q613a9 caenorhabdi
77	43	43.9	407	2	Q2XH80_PSEPU	Q2xh80 pseudomonas
78	43	43.9	407	2	Q9R8R0_PSEPU	Q9r8r0 pseudomonas
79	43	43.9	407	2	Q3KFU8_PSEPF	Q3kfu8 pseudomonas
80	43	43.9	407	2	Q4KFY8_PSEF5	Q4kfy8 pseudomonas
81	43	43.9	407	2	Q88FB0_PSEPK	Q88fb0 pseudomonas

82	43	43.9	417	2	Q5V634_HALMA	Q5v634 haloarcula
83	43	43.9	425	2	Q4PJ71_9BACT	Q4pj71 uncultured
84	43	43.9	491	2	Q3VYJ0_9ACTO	Q3vyj0 frankia sp.
85	43	43.9	1358	2	Q4RWU3_TETNG	Q4rwu3 tetraodon n
86	43	43.9	1770	2	Q4VXC5_HUMAN	Q4vxc5 homo sapien
87	43	43.9	1783	2	Q4R9M7_HUMAN	Q4r9m7 homo sapien
88	43	43.9	1797	2	Q4R9M8_HUMAN	Q4r9m8 homo sapien
89	43	43.9	1809	2	Q4R9M9_HUMAN	Q4r9m9 homo sapien
90	43	43.9	1816	1	KIF1B_HUMAN	O60333 homo sapien
91	43	43.9	1816	2	Q4VXC6_HUMAN	Q4vxc6 homo sapien
92	43	43.9	1823	2	Q4VXC4_HUMAN	Q4vxc4 homo sapien
93	43	43.9	2086	2	Q4RVN7_TETNG	Q4rvn7 tetraodon n
94	43	43.9	2867	2	Q3M1N0_ANAVT	Q3m1n0 anabaena va
95	43	43.9	3035	2	O72347_9POTY	O72347 wheat strea
96	43	43.9	3035	2	Q8V1Y3_9POTY	Q8v1y3 wheat strea
97	42.5	43.4	203	2	Q3KJ29_PSEPF	Q3kj29 pseudomonas
98	42.5	43.4	328	2	Q61GN1_CAEBR	Q61gn1 caenorhabdi
99	42.5	43.4	601	2	Q7V0S7_PROMP	Q7v0s7 prochloroco
100	42.5	43.4	3302	2	Q6E7K0_9CYAN	Q6e7k0 lyngbya maj
101	42	42.9	146	2	Q7UML9_RHOBA	Q7uml9 rhodopirell
102	42	42.9	160	2	Q62L64_BURMA	Q62l64 burkholderi
103	42	42.9	286	2	Q84FA4_MYXXA	Q84fa4 myxococcus
104	42	42.9	334	2	Q9K9C0_BACHD	Q9k9c0 bacillus ha
105	42	42.9	372	2	Q3NLC7_SHEFR	Q3nlc7 shewanella
106	42	42.9	380	2	Q7MB58_PHOLL	Q7mb58 photorhabdu
107	42	42.9	406	2	Q48K70_PSE14	Q48k70 pseudomonas
108	42	42.9	406	2	Q883Z6_PSESM	Q883z6 pseudomonas
109	42	42.9	411	2	Q4ZUW9_PSEU2	Q4zuw9 pseudomonas
110	42	42.9	417	2	Q73KZ4_TREDE	Q73kz4 treponema d
111	42	42.9	592	2	Q4D1I2_TRYCR	Q4d1i2 trypanosoma
112	42	42.9	592	2	Q4PQV7_TRYCR	Q4pqv7 trypanosoma
113	42	42.9	604	2	Q4DB33_TRYCR	Q4db33 trypanosoma
114	42	42.9	741	2	Q6C6E3_YARLI	Q6c6e3 yarrowia li
115	42	42.9	764	2	Q4H3D3_CIOIN	Q4h3d3 ciona intes
116	42	42.9	890	2	Q4RHB2_TETNG	Q4rhb2 tetraodon n
117	42	42.9	1642	1	CO3_NAJKA	Q91132 naja kaouth
118	42	42.9	1652	2	Q49HM6_AUSSU	Q49hm6 austrelaps
119	41	41.8	50	2	Q5NLX0_ZYMMO	Q5nlx0 zymomonas m
120	41	41.8	123	2	Q8IEA5_PLAF7	Q8iea5 plasmodium
121	41	41.8	245	2	Q42A77_DESHA	Q42a77 desulfitoba
122	41	41.8	285	2	Q3APA2_CHLCH	Q3apa2 chlorobium
123	41	41.8	297	2	Q91RF1_9RHAB	Q91rf1 rabies viru
124	41	41.8	299	2	Q668J5_YERPS	Q668j5 yersinia ps
125	41	41.8	299	2	Q8ZCG6_YERPE	Q8zcg6 yersinia pe
126	41	41.8	304	2	Q8D0X2_YERPE	Q8d0x2 yersinia pe
127	41	41.8	307	2	Q6AF34_LEIXX	Q6af34 leifsonia x
128	41	41.8	315	2	Q74SG1_YERPE	Q74sg1 yersinia pe
129	41	41.8	324	2	Q7NNF8_GLOVI	Q7nnf8 gloeobacter
130	41	41.8	343	2	Q6D8W8_ERWCT	Q6d8w8 erwinia car
131	41	41.8	348	2	Q5KXQ7_GEOKA	Q5kxq7 geobacillus
132	41	41.8	349	2	Q43Q58_SOLUS	Q43q58 solibacter
133	41	41.8	358	2	Q8EAI6_SHEON	Q8eai6 shewanella
134	41	41.8	384	1	GAL1_VIBF1	Q5e0m1 vibrio fisc
135	41	41.8	390	2	O85598_BRUAB	O85598 brucella ab
136	41	41.8	392	2	Q3AC11_CARHZ	Q3ac11 carboxydoth
137	41	41.8	397	2	Q2YZN7_9DELT	Q2yzn7 uncultured
138	41	41.8	398	2	Q7RJ04_PLAYO	Q7rj04 plasmodium
139	41	41.8	401	2	Q59X24_CANAL	Q59x24 candida alb
140	41	41.8	419	2	Q4YUY2_PLABE	Q4yuy2 plasmodium
141	41	41.8	444	2	Q50ZU7_ENTHI	Q50zu7 entamoeba h
142	41	41.8	488	2	Q7NW11_CHRVO	Q7nw11 chromobacte

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OM protein - protein search, using sw model

Run on: July 10, 2006, 15:59:05 ; Search time 88.5 Seconds
 (without alignments)
 92.993 Million cell updates/sec

Title: US-10-519-890-16
 Perfect score: 98
 Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

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 2: geneseqp1990s:*
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 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	98	100.0	18	8 ADI29062	Adi29062 Human ins
2	93	94.9	18	8 ADI29048	Adi29048 Human ins
3	93	94.9	18	8 ADI29060	Adi29060 Human ins
4	93	94.9	23	8 ADI29051	Adi29051 Human ins
5	93	94.9	35	3 AAB09734	Aab09734 IGFBP-2 I
6	93	94.9	36	3 AAB09735	Aab09735 IGFBP-2 I
7	93	94.9	37	3 AAB09736	Aab09736 IGFBP-2 I
8	93	94.9	39	3 AAB09761	Aab09761 IGFBP-2 I
9	93	94.9	47	3 AAB09628	Aab09628 Insulin l
10	93	94.9	47	3 AAB09668	Aab09668 IGFBP-2 I
11	93	94.9	52	3 AAB09660	Aab09660 IGFBP-2 I
12	93	94.9	53	3 AAB09659	Aab09659 IGFBP-2 I

13	93	94.9	54	3	AAB09658	Aab09658	IGFBP-2	I
14	93	94.9	54	3	AAB09657	Aab09657	IGFBP-2	I
15	93	94.9	55	3	AAB09661	Aab09661	IGFBP-2	I
16	93	94.9	55	3	AAB09655	Aab09655	IGFBP-2	I
17	93	94.9	55	3	AAB09656	Aab09656	IGFBP-2	I
18	93	94.9	56	3	AAB09653	Aab09653	IGFBP-2	I
19	93	94.9	56	3	AAB09654	Aab09654	IGFBP-2	I
20	93	94.9	57	3	AAB09652	Aab09652	IGFBP-2	I
21	93	94.9	57	3	AAB09662	Aab09662	IGFBP-2	I
22	93	94.9	57	3	AAB09651	Aab09651	IGFBP-2	I
23	93	94.9	58	3	AAB09649	Aab09649	IGFBP-2	I
24	93	94.9	58	3	AAB09650	Aab09650	IGFBP-2	I
25	93	94.9	59	3	AAB09647	Aab09647	IGFBP-2	I
26	93	94.9	59	3	AAB09648	Aab09648	IGFBP-2	I
27	93	94.9	59	3	AAB09663	Aab09663	IGFBP-2	I
28	93	94.9	60	3	AAB09645	Aab09645	IGFBP-2	I
29	93	94.9	60	3	AAB09646	Aab09646	IGFBP-2	I
30	93	94.9	61	3	AAB09643	Aab09643	IGFBP-2	I
31	93	94.9	61	3	AAB09664	Aab09664	IGFBP-2	I
32	93	94.9	61	3	AAB09644	Aab09644	IGFBP-2	I
33	93	94.9	62	3	AAB09641	Aab09641	IGFBP-2	I
34	93	94.9	62	3	AAB09642	Aab09642	IGFBP-2	I
35	93	94.9	63	3	AAB09639	Aab09639	IGFBP-2	I
36	93	94.9	63	3	AAB09640	Aab09640	IGFBP-2	I
37	93	94.9	64	3	AAB09638	Aab09638	IGFBP-2	I
38	93	94.9	64	3	AAB09637	Aab09637	IGFBP-2	I
39	93	94.9	64	3	AAB09627	Aab09627	Insulin	l
40	93	94.9	64	3	AAB09665	Aab09665	IGFBP-2	I
41	93	94.9	65	3	AAB09636	Aab09636	IGFBP-2	I
42	93	94.9	65	3	AAB09635	Aab09635	IGFBP-2	I
43	93	94.9	66	3	AAB09633	Aab09633	IGFBP-2	I
44	93	94.9	66	3	AAB09634	Aab09634	IGFBP-2	I
45	93	94.9	67	3	AAB09632	Aab09632	IGFBP-2	I
46	93	94.9	76	3	AAB09624	Aab09624	Insulin	l
47	93	94.9	76	3	AAB09748	Aab09748	IGFBP-2	I
48	93	94.9	101	3	AAB09626	Aab09626	Insulin	l
49	93	94.9	101	3	AAB09667	Aab09667	IGFBP-2	I
50	93	94.9	105	9	AED74029	Aed74029	Human pla	
51	93	94.9	123	2	AAY25505	Aay25505	Insulin-l	
52	93	94.9	139	3	AAB09625	Aab09625	Insulin	l
53	93	94.9	139	3	AAB09666	Aab09666	IGFBP-2	I
54	93	94.9	216	5	ABP41894	Abp41894	Human ova	
55	93	94.9	228	3	AAB43616	Aab43616	Human can	
56	93	94.9	278	3	AAB09758	Aab09758	IGFBP-2	a
57	93	94.9	289	3	AAB09623	Aab09623	IGFBP-2	a
58	93	94.9	289	3	AAB09753	Aab09753	IGFBP-2	a
59	93	94.9	289	3	AAB09618	Aab09618	Insulin	l
60	93	94.9	289	4	AAB59879	Aab59879	IGFBP-2	m
61	93	94.9	299	2	AAR04909	Aar04909	Rat bindi	
62	93	94.9	300	7	ADE54199	Ade54199	Rat Prote	
63	93	94.9	304	7	ADE56680	Ade56680	Rat Prote	
64	93	94.9	304	7	ADE56684	Ade56684	Rat Prote	
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66	93	94.9	325	7	ADE58187	Ade58187	Human Pro	
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69	93	94.9	325	8	ADQ82882	Adq82882	Human ins	
70	93	94.9	328	2	AAR04908	Aar04908	EcoRI-Eco	
71	93	94.9	328	2	AAR89272	Aar89272	Insulin	l
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75	93	94.9	328	6	ABP96805	Abp96805	Human	COP
76	93	94.9	328	6	ABB82755	Abb82755	Human	IGF
77	93	94.9	328	6	ABU56585	Abu56585	Lung	canc
78	93	94.9	328	7	ADD14079	Add14079	Human	src
79	93	94.9	328	7	ADE56686	Ade56686	Human	Pro
80	93	94.9	328	7	ADE56682	Ade56682	Human	Pro
81	93	94.9	328	7	ADJ68290	Adj68290	Human	hea
82	93	94.9	328	7	ADN95269	Adn95269	Human	BEC
83	93	94.9	328	8	ADK70455	Adk70455	Respirato	
84	93	94.9	328	8	ADL61308	Adl61308	Human	ins
85	93	94.9	328	8	ADQ20663	Adq20663	Human	sof
86	93	94.9	328	8	ADQ26071	Adq26071	Insulin-l	
87	93	94.9	328	9	ADY54943	Ady54943	Chronic	v
88	93	94.9	328	9	ADZ87324	Adz87324	Human	IGF
89	93	94.9	328	9	AEA47743	Aea47743	Amino	aci
90	93	94.9	328	9	AEB29751	Aeb29751	Human	ins
91	93	94.9	328	9	AED51292	Aed51292	Human	ins
92	93	94.9	367	8	ADR66715	Adr66715	Human	pro
93	93	94.9	367	8	ADR66373	Adr66373	Human	pro
94	88	89.8	18	8	ADI29061	Adi29061	Human	ins
95	88	89.8	34	3	AAB09733	Aab09733	IGFBP-2	I
96	87	88.8	18	8	ADI29063	Adi29063	Human	ins
97	87	88.8	18	8	ADI29064	Adi29064	Human	ins
98	83	84.7	33	3	AAB09732	Aab09732	IGFBP-2	I
99	83	84.7	179	5	ABP42224	Abp42224	Human	ova
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102	71	72.4	31	3	AAB09730	Aab09730	IGFBP-2	I
103	67	68.4	30	3	AAB09729	Aab09729	IGFBP-2	I
104	66	67.3	322	8	ADO70022	Ado70022	Human	ins
105	63	64.3	29	3	AAB09728	Aab09728	IGFBP-2	I
106	63	64.3	30	3	AAB09630	Aab09630	Insulin	l
107	63	64.3	41	3	AAB09629	Aab09629	Insulin	l
108	63	64.3	41	3	AAB09669	Aab09669	IGFBP-2	I
109	63	64.3	56	3	AAB09670	Aab09670	IGFBP-2	I
110	58	59.2	28	3	AAB09727	Aab09727	IGFBP-2	I
111	57	58.2	45	3	AAB09687	Aab09687	Insulin	l
112	54	55.1	14	7	ADO32208	Ado32208	Peptide	o
113	54	55.1	14	8	ADO07254	Ado07254	Peptide	B
114	54	55.1	14	8	ADS74123	Ads74123	Peptide	B
115	53	54.1	10	3	AAB09767	Aab09767	IGFBP-2	I
116	53	54.1	27	3	AAB09726	Aab09726	IGFBP-2	I
117	49	50.0	14	3	AAB09672	Aab09672	IGFBP-2	I
118	47	48.0	10	3	AAB09765	Aab09765	IGFBP-2	I
119	47	48.0	51	4	AAB48120	Aab48120	Consensus	
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122	46	46.9	88	4	AAO08527	Aao08527	Human	pol
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128	46	46.9	258	1	AAP93154	Aap93154	Insulin-l	
129	46	46.9	259	1	AAP91868	Aap91868	Recombina	
130	46	46.9	259	6	ABB82754	Abb82754	Human	IGF
131	46	46.9	259	6	ABB82757	Abb82757	Human	IGF
132	46	46.9	259	8	ADE76944	Ade76944	Human	pro
133	46	46.9	259	8	ADH17058	Adh17058	Human	ins
134	46	46.9	259	8	ADL12500	Adl12500	Human	ste

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:03:03 ; Search time 34.5 Seconds
 (without alignments)
 45.668 Million cell updates/sec

Title: US-10-519-890-16
 Perfect score: 98
 Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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1	93	94.9	328	2	US-09-253-316-28	Sequence 28, Appl
2	93	94.9	328	2	US-09-961-403-2	Sequence 2, Appli
3	93	94.9	328	7	5212074-4	Patent No. 5212074
4	54	55.1	14	2	US-10-215-759-14	Sequence 14, Appl
5	54	55.1	14	2	US-10-264-672-14	Sequence 14, Appl
6	54	55.1	14	2	US-10-383-999-14	Sequence 14, Appl
7	46	46.9	259	2	US-09-253-316-27	Sequence 27, Appl
8	46	46.9	259	2	US-09-976-594-229	Sequence 229, App
9	46	46.9	259	2	US-09-919-039-109	Sequence 109, App
10	46	46.9	259	2	US-09-949-001-17	Sequence 17, Appl
11	46	46.9	259	7	5212074-3	Patent No. 5212074
12	46	46.9	314	2	US-09-949-001-23	Sequence 23, Appl
13	43	43.9	301	2	US-09-543-681A-7708	Sequence 7708, Ap
14	42	42.9	170	2	US-09-902-540-11882	Sequence 11882, A
15	42	42.9	1642	1	US-08-447-411-45	Sequence 45, Appl

16	42	42.9	1642	1	US-08-662-227-2	Sequence 2, Appli
17	42	42.9	1642	2	US-09-017-947-2	Sequence 2, Appli
18	42	42.9	1642	2	US-09-925-442-2	Sequence 2, Appli
19	42	42.9	1648	1	US-08-662-227-35	Sequence 35, Appl
20	42	42.9	1648	2	US-09-017-947-35	Sequence 35, Appl
21	42	42.9	1648	2	US-09-925-442-35	Sequence 35, Appl
22	41	41.8	298	2	US-09-248-796A-18012	Sequence 18012, A
23	41	41.8	522	2	US-09-543-681A-5830	Sequence 5830, Ap
24	41	41.8	2079	2	US-09-949-016-8301	Sequence 8301, Ap
25	40	40.8	92	2	US-09-673-395A-285	Sequence 285, App
26	40	40.8	227	1	US-08-829-027-4	Sequence 4, Appli
27	40	40.8	227	2	US-09-225-366-4	Sequence 4, Appli
28	40	40.8	1651	1	US-08-447-411-2	Sequence 2, Appli
29	39	39.8	237	7	5212074-7	Patent No. 5212074
30	39	39.8	258	2	US-09-949-016-6093	Sequence 6093, Ap
31	39	39.8	287	2	US-09-949-016-9099	Sequence 9099, Ap
32	39	39.8	317	2	US-09-949-016-8185	Sequence 8185, Ap
33	39	39.8	337	2	US-09-902-540-16643	Sequence 16643, A
34	39	39.8	395	2	US-09-198-452A-790	Sequence 790, App
35	39	39.8	397	2	US-09-438-185A-742	Sequence 742, App
36	39	39.8	400	2	US-09-270-767-44593	Sequence 44593, A
37	39	39.8	428	2	US-09-799-978-36	Sequence 36, Appl
38	39	39.8	675	2	US-09-591-095-8	Sequence 8, Appli
39	39	39.8	1603	2	US-09-949-016-6136	Sequence 6136, Ap
40	39	39.8	1609	2	US-09-949-016-10910	Sequence 10910, A
41	38	38.8	93	2	US-08-975-040-24	Sequence 24, Appl
42	38	38.8	104	2	US-09-270-767-58263	Sequence 58263, A
43	38	38.8	158	2	US-09-270-767-42940	Sequence 42940, A
44	38	38.8	183	2	US-09-621-976-4209	Sequence 4209, Ap
45	38	38.8	209	2	US-09-461-325-468	Sequence 468, App
46	38	38.8	209	2	US-10-012-542-468	Sequence 468, App
47	38	38.8	209	2	US-10-115-123-468	Sequence 468, App
48	38	38.8	273	2	US-09-949-016-7047	Sequence 7047, Ap
49	38	38.8	317	1	US-08-190-802A-27	Sequence 27, Appl
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51	38	38.8	317	1	US-08-190-802A-47	Sequence 47, Appl
52	38	38.8	317	2	US-08-477-346-27	Sequence 27, Appl
53	38	38.8	317	2	US-08-477-346-41	Sequence 41, Appl
54	38	38.8	317	2	US-08-477-346-47	Sequence 47, Appl
55	38	38.8	317	2	US-08-473-089-27	Sequence 27, Appl
56	38	38.8	317	2	US-08-473-089-41	Sequence 41, Appl
57	38	38.8	317	2	US-08-473-089-47	Sequence 47, Appl
58	38	38.8	317	2	US-08-487-072A-27	Sequence 27, Appl
59	38	38.8	317	2	US-08-487-072A-41	Sequence 41, Appl
60	38	38.8	317	2	US-08-487-072A-47	Sequence 47, Appl
61	38	38.8	317	2	US-09-538-092-1009	Sequence 1009, Ap
62	38	38.8	317	3	US-10-329-258-4	Sequence 4, Appli
63	38	38.8	378	1	US-08-707-793A-4	Sequence 4, Appli
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65	38	38.8	434	2	US-09-538-092-103	Sequence 103, App
66	38	38.8	495	2	US-09-252-991A-19330	Sequence 19330, A
67	38	38.8	524	2	US-09-248-796A-20498	Sequence 20498, A
68	38	38.8	619	2	US-09-457-040B-9	Sequence 9, Appli
69	38	38.8	622	2	US-09-270-767-46333	Sequence 46333, A
70	38	38.8	865	2	US-09-417-197-111	Sequence 111, App
71	38	38.8	871	2	US-09-417-197-109	Sequence 109, App
72	38	38.8	919	1	US-08-788-674-4	Sequence 4, Appli
73	38	38.8	951	2	US-08-816-346-58	Sequence 58, Appl
74	38	38.8	951	2	US-09-335-411-58	Sequence 58, Appl
75	38	38.8	952	1	US-08-788-674-5	Sequence 5, Appli
76	38	38.8	952	2	US-08-816-346-4	Sequence 4, Appli

77	38	38.8	952	2	US-09-335-411-4	Sequence 4, Appli
78	38	38.8	967	2	US-08-816-346-56	Sequence 56, Appl
79	38	38.8	967	2	US-09-335-411-56	Sequence 56, Appl
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81	38	38.8	968	2	US-09-335-411-2	Sequence 2, Appli
82	37.5	38.3	165	2	US-09-489-039A-9882	Sequence 9882, Ap
83	37	37.8	132	2	US-09-732-210-1687	Sequence 1687, Ap
84	37	37.8	134	2	US-09-489-039A-12144	Sequence 12144, A
85	37	37.8	156	2	US-09-270-767-35189	Sequence 35189, A
86	37	37.8	156	2	US-09-270-767-50406	Sequence 50406, A
87	37	37.8	170	2	US-09-775-925-32	Sequence 32, Appl
88	37	37.8	201	2	US-09-570-214B-13	Sequence 13, Appl
89	37	37.8	241	2	US-09-775-925-8	Sequence 8, Appli
90	37	37.8	323	2	US-09-619-353-6	Sequence 6, Appli
91	37	37.8	345	2	US-09-543-681A-6792	Sequence 6792, Ap
92	37	37.8	394	2	US-09-270-767-41967	Sequence 41967, A
93	37	37.8	476	2	US-09-328-352-5950	Sequence 5950, Ap
94	37	37.8	483	2	US-09-252-991A-32383	Sequence 32383, A
95	37	37.8	483	2	US-09-385-219A-48	Sequence 48, Appl
96	37	37.8	509	2	US-09-955-732A-14	Sequence 14, Appl
97	37	37.8	509	2	US-09-775-925-6	Sequence 6, Appli
98	37	37.8	548	2	US-09-543-681A-6561	Sequence 6561, Ap
99	37	37.8	820	1	US-08-380-182-23	Sequence 23, Appl
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102	37	37.8	1163	2	US-09-949-016-11047	Sequence 11047, A
103	36	36.7	63	2	US-09-621-976-5664	Sequence 5664, Ap
104	36	36.7	64	2	US-09-513-999C-4670	Sequence 4670, Ap
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106	36	36.7	126	2	US-09-134-001C-3038	Sequence 3038, Ap
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108	36	36.7	137	2	US-09-270-767-40132	Sequence 40132, A
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114	36	36.7	183	2	US-09-489-039A-7793	Sequence 7793, Ap
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118	36	36.7	194	5	PCT-US95-10194-9	Sequence 9, Appli
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125	36	36.7	295	2	US-09-107-433-4125	Sequence 4125, Ap
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127	36	36.7	314	1	US-08-125-077-19	Sequence 19, Appl
128	36	36.7	317	2	US-09-583-110-4998	Sequence 4998, Ap
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131	36	36.7	375	2	US-09-489-039A-7670	Sequence 7670, Ap
132	36	36.7	410	2	US-09-540-236-2495	Sequence 2495, Ap
133	36	36.7	427	2	US-09-902-540-15261	Sequence 15261, A
134	36	36.7	463	1	US-08-162-402B-9	Sequence 9, Appli
135	36	36.7	549	2	US-09-248-796A-20854	Sequence 20854, A
136	36	36.7	562	2	US-09-252-991A-30993	Sequence 30993, A
137	36	36.7	566	2	US-09-328-352-4809	Sequence 4809, Ap

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:03:58 ; Search time 97.5 Seconds
 (without alignments)
 85.517 Million cell updates/sec

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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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 Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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3	93	94.9	228	3	US-09-925-301-1061	Sequence 1061, Ap
4	93	94.9	328	3	US-09-961-403-2	Sequence 2, Appli
5	93	94.9	328	4	US-10-011-859-28	Sequence 28, Appl
6	93	94.9	328	4	US-10-408-765A-96	Sequence 96, Appl
7	93	94.9	328	4	US-10-648-593-232	Sequence 232, App
8	93	94.9	328	4	US-10-706-791-9	Sequence 9, Appli
9	93	94.9	328	5	US-10-723-860-3483	Sequence 3483, Ap
10	93	94.9	328	5	US-10-991-321-28	Sequence 28, Appl
11	93	94.9	328	5	US-10-923-035-36	Sequence 36, Appl
12	93	94.9	328	5	US-10-887-229A-4	Sequence 4, Appli
13	93	94.9	328	5	US-10-756-149-5613	Sequence 5613, Ap
14	93	94.9	328	5	US-10-501-035-268	Sequence 268, App
15	93	94.9	328	6	US-11-149-564-28	Sequence 28, Appl
16	93	94.9	328	6	US-11-169-041-227	Sequence 227, App

17	93	94.9	328	6	US-11-072-175-232	Sequence 232, App
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20	54	55.1	14	4	US-10-264-672-14	Sequence 14, Appl
21	54	55.1	14	4	US-10-383-999-14	Sequence 14, Appl
22	54	55.1	14	6	US-11-031-919-14	Sequence 14, Appl
23	46	46.9	94	4	US-10-400-005-4	Sequence 4, Appli
24	46	46.9	259	3	US-09-919-039-109	Sequence 109, App
25	46	46.9	259	4	US-10-011-859-27	Sequence 27, Appl
26	46	46.9	259	4	US-10-440-464-57	Sequence 57, Appl
27	46	46.9	259	4	US-10-706-791-7	Sequence 7, Appli
28	46	46.9	259	4	US-10-400-005-1	Sequence 1, Appli
29	46	46.9	259	5	US-10-893-315-65	Sequence 65, Appl
30	46	46.9	259	5	US-10-887-229A-2	Sequence 2, Appli
31	46	46.9	259	5	US-10-756-149-5095	Sequence 5095, Ap
32	46	46.9	259	5	US-10-821-234-1561	Sequence 1561, Ap
33	46	46.9	259	6	US-11-149-564-27	Sequence 27, Appl
34	46	46.9	314	5	US-10-893-315-99	Sequence 99, Appl
35	45	45.9	5317	4	US-10-668-767-59	Sequence 59, Appl
36	44	44.9	88	3	US-09-764-891-3371	Sequence 3371, Ap
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38	44	44.9	711	4	US-10-424-599-259955	Sequence 259955,
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41	43	43.9	407	4	US-10-369-493-13871	Sequence 13871, A
42	43	43.9	638	4	US-10-425-115-314451	Sequence 314451,
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44	43	43.9	1338	4	US-10-257-021-30	Sequence 30, Appl
45	43	43.9	1374	4	US-10-291-172-682	Sequence 682, App
46	43	43.9	1374	4	US-10-221-278-682	Sequence 682, App
47	43	43.9	1381	4	US-10-291-172-306	Sequence 306, App
48	43	43.9	1381	4	US-10-221-278-306	Sequence 306, App
49	43	43.9	1381	4	US-10-381-792-1	Sequence 1, Appli
50	43	43.9	1805	4	US-10-287-226-316	Sequence 316, App
51	43	43.9	1823	4	US-10-381-792-2	Sequence 2, Appli
52	42.5	43.4	198	4	US-10-369-493-13897	Sequence 13897, A
53	42	42.9	39	4	US-10-425-115-231462	Sequence 231462,
54	42	42.9	437	5	US-10-450-763-51171	Sequence 51171, A
55	42	42.9	1642	3	US-09-925-442-2	Sequence 2, Appli
56	42	42.9	1642	5	US-10-884-813-4	Sequence 4, Appli
57	42	42.9	1648	3	US-09-925-442-35	Sequence 35, Appl
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59	41	41.8	284	5	US-10-501-282-1226	Sequence 1226, Ap
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62	41	41.8	451	4	US-10-424-599-173619	Sequence 173619,
63	41	41.8	480	4	US-10-282-122A-68494	Sequence 68494, A
64	41	41.8	2115	4	US-10-208-948-4	Sequence 4, Appli
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90	40	40.8	1385	6	US-11-097-143-7206	Sequence 7206, Ap
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93	40	40.8	2505	4	US-10-205-331-20	Sequence 20, Appl
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96	39.5	40.3	104	4	US-10-425-115-263379	Sequence 263379,
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104	39	39.8	134	4	US-10-425-115-220980	Sequence 220980,
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107	39	39.8	183	4	US-10-425-114-37326	Sequence 37326, A
108	39	39.8	188	4	US-10-282-122A-49027	Sequence 49027, A
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116	39	39.8	258	4	US-10-435-696-47	Sequence 47, Appl
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124	39	39.8	339	5	US-10-732-923-11902	Sequence 11902, A
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127	39	39.8	395	4	US-10-289-762-790	Sequence 790, App
128	39	39.8	428	3	US-09-799-978-36	Sequence 36, Appl
129	39	39.8	428	4	US-10-649-852-36	Sequence 36, Appl
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131	39	39.8	446	4	US-10-437-963-203513	Sequence 203513,
132	39	39.8	479	4	US-10-425-114-56543	Sequence 56543, A
133	39	39.8	511	5	US-10-450-763-34370	Sequence 34370, A
134	39	39.8	542	4	US-10-282-122A-55312	Sequence 55312, A
135	39	39.8	549	4	US-10-425-115-296906	Sequence 296906,
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OM protein - protein search, using sw model

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 45.998 Million cell updates/sec

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SUMMARIES

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5	39	39.8	564	6	US-10-449-902-52967	Sequence 52967, A
6	39	39.8	604	6	US-10-953-349-7849	Sequence 7849, Ap
7	39	39.8	623	6	US-10-953-349-7848	Sequence 7848, Ap
8	39	39.8	675	6	US-10-953-349-7847	Sequence 7847, Ap
9	38	38.8	207	7	US-11-197-712-386	Sequence 386, App
10	38	38.8	275	7	US-11-293-697-3286	Sequence 3286, Ap
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13	38	38.8	624	6	US-10-449-902-54158	Sequence 54158, A
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21	36	36.7	276	6	US-10-449-902-34611	Sequence 34611, A
22	36	36.7	280	6	US-10-449-902-31977	Sequence 31977, A
23	36	36.7	320	6	US-10-449-902-30847	Sequence 30847, A
24	36	36.7	360	6	US-10-953-349-21418	Sequence 21418, A
25	36	36.7	400	6	US-10-449-902-42970	Sequence 42970, A
26	36	36.7	401	6	US-10-449-902-44342	Sequence 44342, A
27	36	36.7	405	6	US-10-953-349-21417	Sequence 21417, A
28	36	36.7	406	6	US-10-953-349-21416	Sequence 21416, A
29	36	36.7	415	6	US-10-953-349-21415	Sequence 21415, A
30	36	36.7	430	6	US-10-953-349-8577	Sequence 8577, Ap
31	36	36.7	547	6	US-10-953-349-8576	Sequence 8576, Ap
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33	36	36.7	640	6	US-10-953-349-40224	Sequence 40224, A
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37	36	36.7	697	6	US-10-953-349-40222	Sequence 40222, A
38	36	36.7	746	6	US-10-953-349-2717	Sequence 2717, Ap
39	36	36.7	772	6	US-10-953-349-2716	Sequence 2716, Ap
40	36	36.7	829	6	US-10-953-349-2715	Sequence 2715, Ap
41	35.5	36.2	186	6	US-10-953-349-25121	Sequence 25121, A
42	35.5	36.2	270	6	US-10-953-349-25120	Sequence 25120, A
43	35.5	36.2	302	6	US-10-953-349-25119	Sequence 25119, A
44	35.5	36.2	402	7	US-11-289-102-218	Sequence 218, App
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46	35	35.7	164	7	US-11-315-825-29	Sequence 29, Appl
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54	35	35.7	265	6	US-10-449-902-32346	Sequence 32346, A
55	35	35.7	282	6	US-10-449-902-52303	Sequence 52303, A
56	35	35.7	295	6	US-10-953-349-18040	Sequence 18040, A
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58	35	35.7	334	6	US-10-953-349-18918	Sequence 18918, A
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63	35	35.7	445	6	US-10-449-902-56463	Sequence 56463, A
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65	35	35.7	503	6	US-10-449-902-45896	Sequence 45896, A
66	35	35.7	553	7	US-11-165-586-26	Sequence 26, Appl
67	35	35.7	632	6	US-10-449-902-56080	Sequence 56080, A
68	35	35.7	637	7	US-11-289-102-335	Sequence 335, App
69	35	35.7	664	7	US-11-174-307B-4614	Sequence 4614, Ap
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71	35	35.7	687	6	US-10-449-902-41408	Sequence 41408, A
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73	35	35.7	699	6	US-10-449-902-56398	Sequence 56398, A
74	35	35.7	711	6	US-10-449-902-49517	Sequence 49517, A
75	35	35.7	737	6	US-10-196-749-38	Sequence 38, Appl

76	35	35.7	737	7	US-11-296-092-15	Sequence 15, Appl
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79	34.5	35.2	341	6	US-10-953-349-835	Sequence 835, App
80	34.5	35.2	343	6	US-10-953-349-834	Sequence 834, App
81	34.5	35.2	360	6	US-10-953-349-833	Sequence 833, App
82	34.5	35.2	900	6	US-10-839-442A-22	Sequence 22, Appl
83	34	34.7	164	6	US-10-953-349-25534	Sequence 25534, A
84	34	34.7	172	6	US-10-953-349-25533	Sequence 25533, A
85	34	34.7	189	7	US-11-293-697-3443	Sequence 3443, Ap
86	34	34.7	198	6	US-10-449-902-29036	Sequence 29036, A
87	34	34.7	222	6	US-10-449-902-30843	Sequence 30843, A
88	34	34.7	229	6	US-10-449-902-29327	Sequence 29327, A
89	34	34.7	243	7	US-11-293-697-3403	Sequence 3403, Ap
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91	34	34.7	262	6	US-10-953-349-38302	Sequence 38302, A
92	34	34.7	266	6	US-10-953-349-38301	Sequence 38301, A
93	34	34.7	272	7	US-11-105-233-168	Sequence 168, App
94	34	34.7	291	7	US-11-301-554-333	Sequence 333, App
95	34	34.7	292	6	US-10-953-349-38300	Sequence 38300, A
96	34	34.7	354	6	US-10-449-902-34464	Sequence 34464, A
97	34	34.7	355	6	US-10-449-902-47892	Sequence 47892, A
98	34	34.7	355	6	US-10-449-902-48076	Sequence 48076, A
99	34	34.7	359	6	US-10-953-349-23128	Sequence 23128, A
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103	34	34.7	541	6	US-10-449-902-47025	Sequence 47025, A
104	34	34.7	599	6	US-10-449-902-41572	Sequence 41572, A
105	34	34.7	599	6	US-10-449-902-53037	Sequence 53037, A
106	34	34.7	639	6	US-10-449-902-53967	Sequence 53967, A
107	34	34.7	639	6	US-10-449-902-55962	Sequence 55962, A
108	34	34.7	657	6	US-10-449-902-40797	Sequence 40797, A
109	34	34.7	698	6	US-10-449-902-46109	Sequence 46109, A
110	34	34.7	728	6	US-10-449-902-42713	Sequence 42713, A
111	34	34.7	728	6	US-10-449-902-46228	Sequence 46228, A
112	34	34.7	735	6	US-10-196-749-88	Sequence 88, Appl
113	34	34.7	757	6	US-10-536-440-3	Sequence 3, Appli
114	34	34.7	806	6	US-10-449-902-43949	Sequence 43949, A
115	34	34.7	831	6	US-10-449-902-51780	Sequence 51780, A
116	34	34.7	885	6	US-10-449-902-47114	Sequence 47114, A
117	33.5	34.2	63	6	US-10-449-902-35108	Sequence 35108, A
118	33.5	34.2	182	6	US-10-449-902-51584	Sequence 51584, A
119	33.5	34.2	327	6	US-10-953-349-5068	Sequence 5068, Ap
120	33.5	34.2	388	6	US-10-953-349-5067	Sequence 5067, Ap
121	33.5	34.2	477	6	US-10-953-349-5434	Sequence 5434, Ap
122	33.5	34.2	500	6	US-10-953-349-5433	Sequence 5433, Ap
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124	33.5	34.2	505	6	US-10-953-349-5432	Sequence 5432, Ap
125	33.5	34.2	548	6	US-10-449-902-47226	Sequence 47226, A
126	33.5	34.2	1357	6	US-10-449-902-49437	Sequence 49437, A
127	33	33.7	17	7	US-11-134-871-441	Sequence 441, App
128	33	33.7	53	6	US-10-471-571A-3836	Sequence 3836, Ap
129	33	33.7	125	6	US-10-953-349-39597	Sequence 39597, A
130	33	33.7	127	6	US-10-953-349-6937	Sequence 6937, Ap
131	33	33.7	189	6	US-10-449-902-42125	Sequence 42125, A
132	33	33.7	218	6	US-10-953-349-39596	Sequence 39596, A
133	33	33.7	220	6	US-10-953-349-6936	Sequence 6936, Ap
134	33	33.7	230	6	US-10-953-349-39595	Sequence 39595, A
135	33	33.7	240	6	US-10-953-349-6935	Sequence 6935, Ap
136	33	33.7	247	7	US-11-197-712-346	Sequence 346, App

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OM protein - protein search, using sw model

Run on: July 10, 2006, 16:02:44 ; Search time 18.75 Seconds
 (without alignments)
 92.368 Million cell updates/sec

Title: US-10-519-890-16
 Perfect score: 98
 Sequence: 1 KHGLYNLAQCKMSLNGQR 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	93	94.9	304	2	A33274	insulin-like growt
2	93	94.9	310	2	A60967	insulin-like growt
3	93	94.9	317	2	I46916	insulin-like growt
4	93	94.9	328	1	A41927	insulin-like growt
5	87	88.8	305	2	JN0508	insulin-like growt
6	87	88.8	305	2	I48601	insulin-like growt
7	48	49.0	236	2	T45067	hypothetical prote
8	48	49.0	272	1	A36082	insulin-like growt
9	47	48.0	263	1	S23009	insulin-like growt
10	46	46.9	259	1	IOHU1	insulin-like growt
11	45	45.9	272	2	I48600	insulin-like growt
12	42	42.9	334	2	A83991	glycolate oxidase
13	42	42.9	1642	2	I51018	cobra venom factor
14	41	41.8	299	2	AH0367	conserved hypothet
15	41	41.8	830	2	T04848	protein kinase hom
16	41	41.8	2143	2	G96595	hypothetical prote
17	40	40.8	227	2	JQ1945	nucleoside-triphos
18	40	40.8	949	2	A81138	excinnuclease ABC c

19	40	40.8	949	2	E75352	glycine cleavage s
20	40	40.8	1651	1	C3NJ	complement C3 prec
21	40	40.8	2505	1	XYRTFA	enoyl-[acyl-carrie
22	39.5	40.3	444	2	E96905	TPR-repeat-contain
23	39.5	40.3	1557	2	T28811	hypothetical prote
24	39	39.8	214	2	JQ2001	hypothetical 24K p
25	39	39.8	237	2	I47031	insulin-like growt
26	39	39.8	254	2	I48603	insulin-like growt
27	39	39.8	254	2	I48599	insulin-like growt
28	39	39.8	254	2	JC1464	insulin-like growt
29	39	39.8	258	1	B37252	insulin-like growt
30	39	39.8	258	2	A45403	insulin-like growt
31	39	39.8	353	2	D96596	hypothetical prote
32	39	39.8	395	2	A86583	aromatic AA aminot
33	39	39.8	395	2	B72042	aromatic-amino-aci
34	39	39.8	419	2	G86198	hypothetical prote
35	39	39.8	456	2	F88493	protein F57B9.9 [i
36	39	39.8	522	2	S33029	hypothetical prote
37	39	39.8	542	2	B81662	apolipoprotein N-a
38	39	39.8	619	2	E82765	DNA mismatch repai
39	39	39.8	879	2	B84765	hypothetical prote
40	39	39.8	915	1	A48225	subtilisin-like pr
41	39	39.8	915	2	B48225	probable proprotei
42	39	39.8	1239	1	VHWVEE	structural polypro
43	39	39.8	1240	1	VHWVEV	structural polypro
44	39	39.8	1241	2	S26373	genome polyprotein
45	39	39.8	1242	2	A56605	structural polypro
46	39	39.8	1242	2	S72350	structural polypro
47	39	39.8	1256	2	S14556	asparagine-rich pr
48	39	39.8	1403	2	T49093	hypothetical prote
49	39	39.8	1548	2	S34583	serine proteinase
50	39	39.8	1603	2	S23810	collagen alpha 1(X
51	39	39.8	2895	2	T08437	hyperplastic discs
52	38.5	39.3	132	2	D72616	hypothetical prote
53	38.5	39.3	333	1	H86381	probable acid phos
54	38	38.8	317	2	S45054	GTP-binding regula
55	38	38.8	317	2	S38398	GTP-binding regula
56	38	38.8	317	2	A33928	GTP-binding protei
57	38	38.8	317	2	B33928	GTP-binding protei
58	38	38.8	317	2	A36986	activated protein
59	38	38.8	344	2	T37277	probable cathepsin
60	38	38.8	362	2	S71071	site-specific DNA-
61	38	38.8	428	2	A83494	hypothetical prote
62	38	38.8	434	2	S67639	26S proteasome reg
63	38	38.8	465	2	F65207	hydH protein - Esc
64	38	38.8	484	2	T16695	hypothetical prote
65	38	38.8	618	2	I48914	protein-tyrosine k
66	38	38.8	619	2	A44266	protein-tyrosine k
67	38	38.8	624	2	T48587	peptide transporte
68	38	38.8	647	2	A37086	beta-galactosidase
69	38	38.8	803	2	T24685	hypothetical prote
70	38	38.8	846	2	T39261	amp deaminase - fi
71	38	38.8	919	2	S33942	hexon protein - hu
72	38	38.8	923	1	HXAD40	hexon protein - hu
73	38	38.8	925	1	HXAD41	hexon protein - hu
74	38	38.8	936	2	S57637	hexon protein - hu
75	38	38.8	937	2	S55504	hexon protein - hu
76	38	38.8	937	2	S39301	hexon protein - hu
77	38	38.8	940	2	S37216	hexon protein - hu
78	38	38.8	942	2	S39298	hexon protein - hu
79	38	38.8	952	1	HXAD5	hexon protein - hu

80	38	38.8	967	1	HXAD2	hexon protein - hu
81	38	38.8	996	2	T10725	protein kinase Xa2
82	38	38.8	1286	2	T18734	hypothetical prote
83	38	38.8	1434	2	C82923	DNA-directed RNA p
84	37.5	38.3	264	2	AI0439	conserved hypothet
85	37.5	38.3	404	2	S12209	pectate lyase (EC
86	37.5	38.3	3133	2	S52093	hemocytin - silkwo
87	37	37.8	33	2	A55998	brevinin-2Ea - edi
88	37	37.8	117	2	F70074	hypothetical prote
89	37	37.8	132	2	T38486	probable ribosomal
90	37	37.8	134	2	H84726	hypothetical prote
91	37	37.8	145	2	S36244	fimA protein - Bor
92	37	37.8	207	2	E90140	hypothetical prote
93	37	37.8	236	2	AF2927	transcription regu
94	37	37.8	262	2	A98355	transcription regu
95	37	37.8	363	2	C83128	2,3-butanediol deh
96	37	37.8	394	2	D69370	probable acyl-CoA
97	37	37.8	465	2	T29257	hypothetical prote
98	37	37.8	477	2	AC0903	Penicillin-binding
99	37	37.8	477	2	H85981	D-alanyl-D-alanine
100	37	37.8	477	2	E91136	D-alanyl-D-alanine
101	37	37.8	477	2	A54535	serine-type D-Ala-
102	37	37.8	482	2	AC0426	serine-type D-Ala-
103	37	37.8	554	2	E97852	hypothetical prote
104	37	37.8	602	2	H86468	protein F12K21.20
105	37	37.8	604	2	F87244	replicative DNA he
106	37	37.8	608	2	D72306	hypothetical prote
107	37	37.8	707	2	T28418	ORF MSV257 leucine
108	37	37.8	819	2	AH0056	aspartate kinase (
109	37	37.8	820	1	DEECK	thrA bifunctional
110	37	37.8	820	2	B85480	aspartokinase I, h
111	37	37.8	820	2	B90629	aspartokinase I-ho
112	37	37.8	820	2	AC0502	aspartokinase I/ho
113	37	37.8	1018	2	T43168	hypothetical prote
114	37	37.8	1139	2	T33368	hypothetical prote
115	37	37.8	1158	2	S57348	nuclear factor RIP
116	37	37.8	1217	2	T00607	hypothetical prote
117	37	37.8	1259	2	T16038	hypothetical prote
118	37	37.8	1282	2	T30577	DNA topoisomerase
119	37	37.8	5126	2	S40450	ryanodine receptor
120	36.5	37.2	125	2	F64685	hypothetical prote
121	36.5	37.2	125	2	A71831	hypothetical prote
122	36.5	37.2	229	2	B69712	mutants block spor
123	36.5	37.2	359	1	ADRFAS	fructose-bisphosph
124	36.5	37.2	403	2	JC5269	neuron-specific si
125	36	36.7	71	2	AG0507	conserved hypothet
126	36	36.7	118	2	D89951	50S ribosomal prot
127	36	36.7	148	2	T28287	ORF MSV126 hypothe
128	36	36.7	150	2	A95197	conserved hypothet
129	36	36.7	150	2	F98063	hypothetical prote
130	36	36.7	173	2	T06103	hypothetical prote
131	36	36.7	186	2	AI3292	protein translatio
132	36	36.7	211	2	C83360	hypothetical prote
133	36	36.7	232	2	C83139	outer membrane pro
134	36	36.7	249	2	JC6191	ATP-binding casset
135	36	36.7	262	2	B90099	hypothetical prote
136	36	36.7	265	1	MNVNIM	nonstructural prot
137	36	36.7	265	1	MNVNV4	nonstructural prot
138	36	36.7	273	2	PC4153	monophenol monooxy
139	36	36.7	283	2	T26448	hypothetical prote
140	36	36.7	286	2	B95011	hypothetical prote